# Supplementary Materials

**Table S1.** Nucleotide accession numbers of sequences used for *fdhF* primer design (see Fig. 1).

| Source | Accession Number [1] |
|---|---|
| *Aeromonas salmonicida* subsp. *salmonicida* A449 | NC_009348.1:1906100-1908244 |
| *Aggregatibacter aphrophilus* NJ8700 | NC_012913.1: c1159571-1157412 |
| *Citrobacter koseri* ATCC BAA-895 copy 1 | NC_009792.1:3531364-3533511 |
| *Citrobacter koseri* ATCC BAA-895 copy 2 | NC_009792.1:1727418-1729565 |
| *Citrobacter rodentium* ICC168 copy 1 | NC_013716.1:c3662542-3660395 |
| *Citrobacter rodentium* ICC168 copy 2 | NC_013716.1:c3568359-3566212 |
| *Citrobacter* sp. 30_2 copy 1 | NZ_GG657366.1:c93031-90884 |
| *Citrobacter* sp. 30_2 copy 2 | NZ_GG657366.1:c1094197-1096347 |
| *Citrobacter youngae* ATCC 29220 copy 1 | NZ_ABWL01000021.1:c93031-90884 |
| *Citrobacter youngae* ATCC 29220 copy 2 | NZ_ABWL01000021.1:c24883-27030 |
| *Clostridium bartlettii* DSM 16795 | NZ_ABEZ02000007.1:c36324-34174 |
| *Clostridium beijerinckii* NCIMB 8052 | NC_009617.1:c4364248-4366389 |
| *Clostridium bolteae* ATCC BAA-613 | NZ_ABCC02000017.1:93731-95716 |
| *Clostridium carboxidivorans* P7 copy 1 | NZ_ACVI01000105.1:231-2378 |
| *Clostridium carboxidivorans* P7 copy 2 | NZ_ACVI01000010.1:36001-38157 |
| *Clostridium difficile* 630 | NC_009089.1:c3884230-3882086 |
| *Cronobacter sakazakii* ATCC BAA-894 | NC_009778.1:c1996280-1998430 |
| *Cronobacter turicensis* copy 1 | NC_013282.1:2002311-2004458 |
| *Cronobacter turicensis* copy 2 | NC_013282.1:1996635-1998845 |
| *Dickeya dadantii* Ech586 | NC_013592.1:2958853-2961003 |
| *Dickeya dadantii* Ech703 | NC_012880.1:c1450903-1453053 |
| *Dickeya zeae* Ech1591 | NC_012912.1:3084906-3087056 |
| *Edwardsiella ictaluri* 93-146 | NC_012779.1:3156478-3158622 |
| *Edwardsiella tarda* EIB202 | NC_013508.1:3053142-3055286 |
| *Enterobacter cancerogenus* ATCC 35316 | NZ_ABWM02000022.1:21042-23189 |
| *Enterobacter* sp. 638 copy 1 | NC_009436.1:c 329787-331934 |
| *Enterobacter* sp. 638 copy 2 | NC_009436.1:c1907448-1909598 |
| *Escherichia coli* K-12 substr MG1655 | NC_000913.2:c4295242-4297389 |
| *Escherichia fergusonii* ATCC 35469 | NC_011740.1:4397249-4399396 |
| *Klebsiella pneumoniae* NTXH-K2044 copy 1 | NC_012731.1:c358869-356722 |
| *Klebsiella pneumoniae* NTXH-K2044 copy 2 | NC_012731.1:3017444-3019594 |
| *Pantoea* sp. At-9b | NZ_ACYJ01000001:122540-124690 |
| *Pectobacterium atrosepticum* SCRI1043 copy 1 | NC_004547.2:c1752061-1754157 |
| *Pectobacterium atrosepticum* SCRI1043 copy 2 | NC_004547.2:1420602-1422752 |
| *Pectobacterium carotovorum* sbsp. carotovorum WPP14 | NZ_ABVY01000027.1:c9266-11416 |
| *Pectobacterium wasabiae* WPP163 | NC_013421.1:c1930748-1932898 |
| *Photobacterium profundum* 3TCK | NZ_AAPH01000003.1:97396-99486 |
| *Proteus mirabilis* HI4320 copy 1 | NC_010554.1:3909884-3912028 |

| | |
|---|---|
| *Proteus mirabilis* HI4320 copy 2 | NC_010554.1:c3265604-3267772 |
| *Providencia alcalifaciens* DSM 30120 | NZ_ABXW01000042.1:35044-37197 |
| *Providencia rustigianii* DSM 4541 | NZ_ABXV02000023.1:88004-90157 |
| *Psychromonas* sp. CNPT3 | NZ_AAPG01000013.1:c3595-5742 |
| *Salmonella enterica* sbsp. enterica serovar Typhi CT18 | NP_458584; NC_003198.1:4370484-4372631 |
| *Salmonella typhimurium* LT2 | NP_463150; NC_003197.1:c4525350-4527497 |
| *Serratia proteamaculans* 568 | NC_009832.1:c2657681-2659837 |
| *Shigella* sp. D9 | NZ_ACDL01000041.1:c37225-39372 |
| *Treponema primitia* str. ZAS-2 copy 1 (Sec FDH) | FJ479768:50505-52697 |
| *Treponema primitia* str. ZAS-2 copy 2 (Cys FDH) | FJ479768:30735-32933 |
| *Vibrio angustum* S14 | NZ_AAOJ01000001.1:c1074316-1076460 |
| *Yersinia aldovae* ATCC 35236 | NZ_ACCB01000002.1:136225-138372 |
| *Yersinia bercovieri* ATCC 43970 | NZ_AALC02000017.1:13658-15805 |
| *Yersinia enterocolitica* subsp. enterocolitica 8081 | NC_008800.1:3050211-3052358 |
| *Yersinia frederiksenii* ATCC 33641 copy 1 | NZ_AALE02000011.1:c133500-135647 |
| *Yersinia frederiksenii* ATCC 33641 copy 2 | NZ_AALE02000004.1:63404-65548 |
| *Yersinia mollaretii* ATCC 43969 copy 1 | NZ_AALD02000005.1:c25400-27571 |
| *Yersinia mollaretii* ATCC 43969 copy 2 | NZ_AALD02000036.1:52-2196 |
| *Yersinia rohdei* ATCC 43380 | NZ_ACCD01000002.1:c116227-118374 |
| *Yersinia ruckeri* ATCC 29473 | NZ_ACCC01000020.1:c42838-44961 |

[1] A 'c' before genome coordinates indicates complementary sequence

**Table S2.** PCR primer combinations and concentrations for *fdhF* amplication from pure culture and insect gut templates. Sequenced amplicons were classified as $fdhF_{Sec}$ ('Sec') or $fdhF_{Cys}$ ('Cys') versions of *fdhF* based on whether their deduced amino acid translations encode a selenocysteine or cysteine, respectively, at the catalytic active site. All templates are DNA unless noted. Primer set 1: fdhF-F1, fdhF-F2, fdhF-F3, fdhF-R1, fdhF-R2. Primer set 2: universal primers EntfdhFunv- F1, TgfdhFunv-F1, and fdhFunv-R1.

| Templates | Primer Combinations (μM final conc.) | Amplicon |
|---|---|---|
| *Treponema primitia* str. ZAS-2 | fdhF-F1 (1.0), fdhF-R1 (1.0) | Sec |
| *T. primitia* str. ZAS-2 | fdhF-F1 (1.0), fdhF-R2 (1.0) | Cys |
| *T. primitia* str. ZAS-1 | fdhF-F1 (1.0), fdhF-R1 (1.0) | Sec |
| *T. primitia* str. ZAS-1 | fdhF-F1 (1.0), fdhF-R2 (1.0) | Cys |
| *Buttiauxiella* sp. SN-1 | fdhF-F3 (1.0), fdhF-R2 (1.0) | Sec |
| *Serratia grimesii* str. ZFX-1 | fdhF-F2 (1.0), fdhF-R1 (1.0) | Cys |
| *Citrobacter* sp. TSA-1 | Primer set 2 forward (0.5), reverse (1.0) | Sec |
| *Acetonema longum* str. APO-1 | Primer set 2 forward (0.5), reverse (1.0) | Sec |
| *Pantoea stewartii subsp. stewartii* | Primer set 2 forward (0.5), reverse (1.0) | no product |
| *Zootermopsis nevadensis* collection ChiA1 gut DNA | Primer set 1 forward (0.3), reverse (0.3) | Sec, Cys |
| *Zootermopsis nevadensis* collection ChiA1 gut DNA | Primer set 2 forward (0.5), reverse (1.0) | Sec, Cys |
| *Zootermopsis nevadensis* collection ChiB gut cDNA | Primer set 2 forward (0.5), reverse (1.0) | Sec, Cys |
| *Reticulitermes hesperus* collection ChiA2 gut DNA | Primer set 2 forward (0.5), reverse (1.0) | Sec, Cys |
| *Incisitermes minor* isolate collection Pas1 gut DNA | Primer set 2 forward (0.5), reverse (1.0) | Sec, Cys |
| *Cryptocercus punctulatus* gut DNA | Primer set 2 forward (1.0), reverse (1.0) | Sec, Cys |

**Table S3.** FDH phylotype distribution in wood-feeding insect gut inventories. Phylotypes (i.e., operational taxonomic units) were identified using DOTUR at a cutoff of 97% protein similarity level (Jones-Thorton-Taylor corrected). The number of genotypes, inferred based on RFLP sorting, comprising each phylotype are listed. PS1: primers fdhF-F1, fdhF-F2, fdhF-F3, fdhF-R1, fdhF-R2. PS 2: universal primers EntfdhFunv-F1, TgfdhFunv-F1, and fdhFunv-R1.

| Clone Library (No. clones, primer set) | Phylotype (No. genotypes) | Abundance |
|---|---|---|
| *Zootermopsis nevadensis* ChiA1 (84, PS 1) | | |
| | Zn9cys (10) | 42.9% |
| | Zn2cys (1) | 22.6% |
| | Zn70sec (6) | 17.9% |
| | Zn62sec (1) | 13.1% |
| | Zn13cys (1) | 1.2% |
| | Zn51sec (1) | 1.2% |
| | Zn61sec (1) | 1.2% |
| *Zootermopsis nevadensis* ChiA1 (86, PS 2) | | |
| | ZnC1cys (2) | 45.3% |
| | ZnD2sec (1) | 23.3% |
| | ZnF7sec (3) | 4.7% |
| | ZnH6cys (2) | 3.5% |
| | ZnB3cys (1) | 3.5% |
| | ZnB5sec (3) | 3.5% |
| | ZnB8sec (1) | 2.3% |
| | ZnC6sec (1) | 2.3% |
| | ZnD3cys (1) | 2.3% |
| | ZnA4cys (2) | 2.3% |
| | ZnC8sec (2) | 2.3% |
| | ZnB9cys (1) | 1.2% |
| | ZnC11cys (1) | 1.2% |
| | ZnE2cys (1) | 1.2% |
| | ZnH8cys (1) | 1.2% |
| *Zootermopsis nevadensis* ChiB (81, PS 2) | | |
| | Zn5secRT (2) | 29.6% |
| | Zn16secRT (2) | 19.8% |
| | Zn2cysRT (3) | 12.3% |
| | Zn25secRT (6) | 11.1% |
| | Zn9cysRT (3) | 6.2% |
| | Zn56secRT (2) | 3.7% |
| | Zn55secRT (1) | 2.5% |
| | Zn67cysRT (1) | 2.5% |
| | Zn71cysRT (1) | 2.5% |
| | Zn75cysRT (3) | 2.5% |
| | Zn76secRT (1) | 2.5% |
| | Zn36secRT (1) | 1.2% |

| | | |
|---|---|---|
| | Zn51secRT (1) | 1.2% |
| | Zn61secRT (1) | 1.2% |
| | Zn72secRT (1) | 1.2% |
| *Reticulitermes hesperus* ChiA2 (89, PS 2) | | |
| | Rh36cys (6) | 30.3% |
| | Rh2sec (5) | 28.1% |
| | Rh9sec (1) | 10.1% |
| | Rh15cys (3) | 7.9% |
| | Rh41sec (5) | 6.7% |
| | Rh24sec (2) | 5.6% |
| | Rh35sec (2) | 2.2% |
| | Rh53sec (2) | 2.2% |
| | Rh54cys (2) | 2.2% |
| | Rh47cys (1) | 1.1% |
| | Rh65cys (1) | 1.1% |
| | Rh71sec (1) | 1.1% |
| | Rh93cys (1) | 1.1% |
| *Incisitermes minor* Pas1 (80, PS 2) | | |
| | Im5cys (5) | 18.8% |
| | Im26sec (3) | 17.5% |
| | Im15sec (5) | 16.3% |
| | Im11cys (7) | 13.8% |
| | Im27sec (2) | 10.0% |
| | Im42cys (2) | 6.3% |
| | Im10sec (2) | 5.0% |
| | Im22sec (1) | 5.0% |
| | Im24cys (2) | 2.5% |
| | Im3sec (1) | 2.5% |
| | Im63sec (2) | 2.5% |
| *Cryptocercus puntulatus nymph* (136, PS 2) | | |
| | Cp16sec (11) | 21.3% |
| | Cp10sec (12) | 17.6% |
| | Cp3sec (4) | 9.6% |
| | CpF1cys (6) | 8.8% |
| | Cp14sec (4) | 8.1% |
| | Cp72cys (4) | 4.4% |
| | CpH1cys (2) | 3.7% |
| | CpD8sec (1) | 2.9% |
| | CpB3sec (3) | 2.9% |
| | Cp9cys (2) | 2.9% |
| | CpB10sec (1) | 2.9% |
| | CpC3sec (2) | 2.9% |
| | CpC1cys (1) | 1.5% |
| | CpD1cys (1) | 1.5% |
| | CpB2sec (1) | 1.5% |
| | CpE8cys (1) | 1.5% |
| | CpF9cys (1) | 1.5% |
| | CpF8cys (1) | 1.5% |
| | Cp28sec (1) | 1.5% |
| | Cp24sec (1) | 1.5% |
| | Cp34sec (1) | 1.5% |

| | |
|---|---|
| Cp78sec (1) | 1.5% |
| Cp82sec (1) | 1.5% |
| Cp94sec (1) | 1.5% |

**Table S4.** Summary of *fdhF* inventories generated from wood-feeding insect guts.

| Clone library templates | Sample Type | No. Clones Analyzed | No. of OTU[1] | Mean Chao1 (SD)[2] | 95% LCI, HCI[3] | No. Sec, Cys OTU[4] |
|---|---|---|---|---|---|---|
| *Zootermopsis nevadensis* collection ChiA1 | DNA | 84 | 7 | 7.53 (1.88) | 6.61, 17.23 | 4, 3 |
| *Zootermopsis nevadensis* collection ChiA1 | DNA | 86 | 15 | 14.96 (2.78) | 13.11, 27.81 | 6, 9 |
| *Zootermopsis nevadensis* collection ChiB | cDNA | 81 | 15 | 14.78 (2.52) | 13.20, 26.79 | 10, 5 |
| *Reticulitermes hesperus* collection ChiA2 | DNA | 89 | 13 | 13.66 (3.86) | 11.49, 33.15 | 7, 6 |
| *Incisitermes minor* isolate collection Pas1 | DNA | 80 | 11 | 10.92 (0.62) | 10.69, 13.6 | 7, 4 |
| *Cryptocercus punctulatus* nymph[5] | DNA | 136 | 24 | 21.52 (2.97) | 21.52, 37.03 | 15, 9 |

[1] Number of operational taxonomic units (OTU) determined using DOTUR (Schloss and Handelsman, 2005) based on > 3% amino acid distance between different phylotypes.
[2] Bias-corrected Chao1 diversity estimator calculated using EstimateS (Colwell, 2009) based on 100 randomizations, sampling without replacement; SD = standard deviation.
[3] Lower (LCI) and higher (HCI) 95% confidence interval limits for mean Chao1 as calculated by EstimateS.
[4] Number of unique Sec and Cys $FDH_H$ phylotypes.
[5] Sequences derived from PCR at different annealing temperatures (51°C and 57 °C) were combined for analyses.

**Table S5.** Amino acid alignment in the area of a characteristic amino acid indel (bold) found only in Gut spirochete group $FDH_H$ sequences. The alignment corresponds to amino acids 394-420 in the selenocysteine encoding $FDH_H$ of *T. primitia* str. ZAS-2. When compared to the protein crystal structure of *E. coli* $FDH_H$ (protein databank identifier 1aa6), the indel was predicted to be located next to an a-helix and hydrogen-bonded turn on the exterior of $FDH_H$. Sequences are listed in phylogenetic order (see Figure 6).

| Sequence | Amino Acid Alignment |
|---|---|
| Zn16secRT | LSDQPGITLTLVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| ZnB8sec | LSDQPGITLTLVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| Zn72secRT | LSDQPGITLTLVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| Zn51sec | LSDQPGITLTLVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| Zn5secRT | LSDQPGITLTLVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| Zn56secRT | LSDKPGITLTLVPHHVL**HEKDP**TKQIHAYYIMGEDPGQSDPD |
| ZnB5sec | LSDKPGITLTLVPHHVL**HEKDP**TKQIHAYYIMGEDPGQSDPD |
| Zn25secRT | LSDKPGITLTAVPHQVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| ZnF7sec | LSDKPGITLTAVPHQVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| ZnC6sec | LSDKAGITLTLVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| Cp94sec | LSDQLGITLTTVPHHVL**HEKDP**KKRIHAYYIMGEGPGQSDPD |
| Cp14sec | LSDQPGITLTVVPHQVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| CpB3sec | LSDQPGITLTVVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| Cp34sec | LSDQPGITLTVVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| Cp82sec | LSDQPGITLTVVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| Cp10sec | LSDQPGITLTVVPHHVL**HEKDP**AKQIHAYYIMGEDPGQSDPD |
| Rh71sec | LSPDVGITLTTVPHQVL**HETDP**KKKIHAYYIMGEDPAQSDPD |
| Rh9sec | LSPDVGITLTTVPHQVL**HETDP**KKQIHAYYIMGEDPAQSDPD |
| Rh24sec | LSADIGITLTTVPHQVL**HEKDP**KKQIHAYYIMGEDPGQSDPD |
| Zn36secRT | LSDQPGITLTTVPHQVL**HETDP**RKQIHAYYIMGEDPGQSDPD |
| Zn51secRT | LSPDLGITLTTVPHQVL**HEKDP**KKQIHAYYIMGEDPGQSDPD |
| Zn61sec | LSPDLGITLTTVPHQVL**HEKDP**KKQIHAYYIMGEDPGQSDSD |
| Cp16sec | LSDKLGITLTTVPHQVL**HETDP**TKQIHAYYIMGEDPGQSDPD |
| Cp3sec | LSDKAGITLTMVPHQVL**AEKDP**AKKIHAYYIMGEDPGQSDPD |
| CpC3sec | LSDKAGTTLTMVPHQVL**AETDP**AKKIHAYYIMGEDPGQSDPD |
| Cp24sec | LSDKPGITLTMVPHQVL**AETDP**AKKIHAYYIMGEDPGQSDPD |
| Cp78sec | LSDKPGITLTMVPHQVL**AETDP**AKKIHAYYIMGEDPGQSDPD |
| *Treponema primitia* str. ZAS-2 fdhFsec | LSDKPGITLTVVPHHVL**HEKDP**TKQIHAYYIMGEDPVQSDPD |
| ZnC8sec | LSDKPGITLTVVPHHVL**HEKDP**TKQIHAYYIMGEDPVQSDPD |
| Zn61secRT | LSDKPGITLTVVPHHVL**HEKDP**TKQIHAYYIMGEDPVQSDPD |

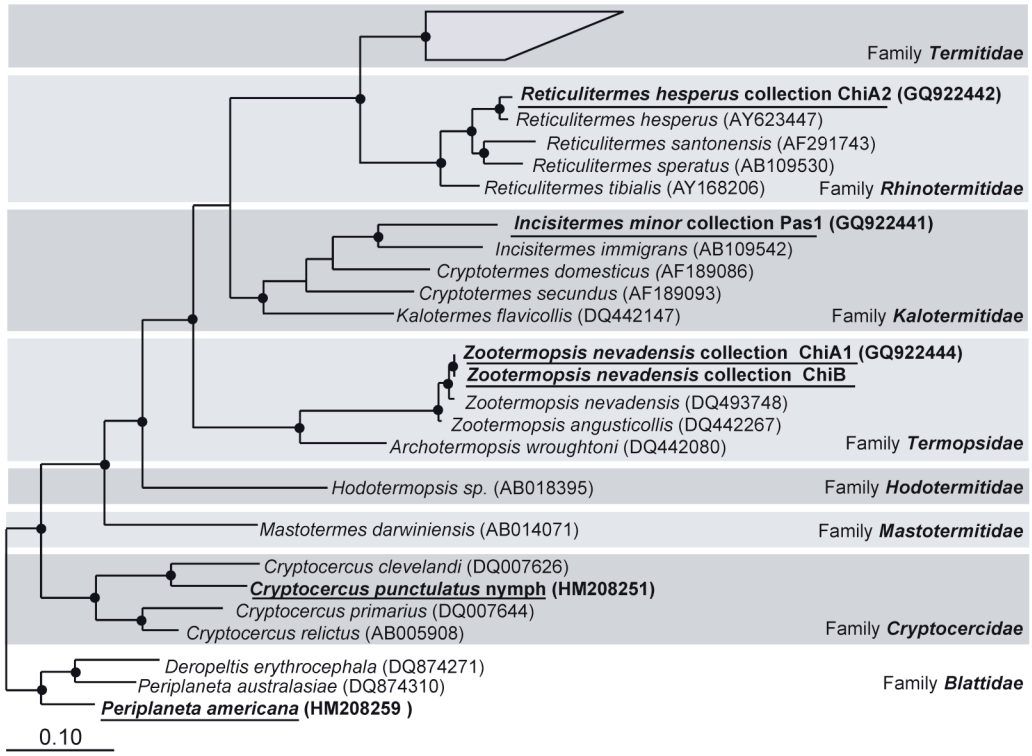
| | |
|---|---|
| Zn70sec | LSDKPGITLTVVPHHVL**HEKDP**TKQIHAYYIMGEDPVQSDPD |
| *Treponema primitia* str. ZAS-1 fdhFsec | LSDKPGITLTVVPHHVL**HETDP**AKQIHAYYIMGEDPVQSDPD |
| CpD8sec | LSDQAGITLTVVPHHVL**HEKDP**AKQIHAYYIMGEDPVQSDPD |
| Zn55secRT | LSDKAGITLTVVPHQVL**HEKDP**KKQIHAYYIMGEDPVQSDPD |
| Rh41sec | LSDQPGITLTVVPHHVL**HETDP**AKQIHAYYIMGEDPAQSDPD |
| Im22sec | LSGEPGITLTTVPQRVL**HEKDP**AKHIRAYYVMGEDPAQSDPD |
| Im26sec | LSDQPGITLTMVPHQVL**HEKDP**AKKIRGYYIMGEDPAQSDPD |
| Im27sec | LSDQPGITLTMVPHHVL**HEKDP**AKQIHAYYVLGEDPAQSDPD |
| Im63sec | LSDQPGITLTMVPHHVL**HEKDP**AKKIRAYYIMGEDPAQSDPD |
| Im10sec | LSDQAGITLTGVPHQVL**HETDP**AKKIRAYYIMGEDPAQSDPD |
| Rh2sec | LPDQNGITLTVVPHQVL**HEKDP**TKQIHGYYIMGEDPVQSDPD |
| Rh35sec | LPDQNGITLTVVPHQVL**HETDP**AKKIHGYYIMGEDPVQSDPD |
| Rh53sec | LPAENGITLTVVPGRVL**HEKDP**SKQIHAYYIMGEDPVQSDPD |
| Zn62sec | LSNKIGIPLTQVPHYVL**HETE-**EKKIRAYYIFGEDPAQSDPD |
| ZnD2sec | LSNKIGIPLTQVPHYVL**HETE-**EKKIRAYYIFGEDPAQSDPD |
| Zn76secRT | LSNKIGIPITQVPRYVL**HEPE-**EKKIRAYYIFGEDPAQSDPD |
| Im3sec | LPEKVGIPLTQVPHYVL**HEPE-**ERKIRAYYVFGEDPAQSDPD |
| CpB2sec | LSDKVGITLTKVPHHVL**HEKG-**AKKIHAYYIMGEDPAQSDPD |
| Im15sec | LSDKVGCPITHVPHRVL**HEKDP**AKRIHAYYIFGEDPAQSDPD |
| ZnC1cys | LDNKVGIQLTRIPEFVI**HEKNP**ANRIHAYYITGEDPAQSDPD |
| ZnHcys | LDNKVGIQLTRIPEFVI**HEKNP**ANRIHAYYITGEDPAQSDPD |
| CpE8cys | LDNKVGIQLTRIPEFVI**HEQDP**AKRIHAYYITGEDPAQSDPD |
| Rh15cys | LDNKVGIQLTRIAEFTI**HQKDP**AKRIHAYYITGEDPAQSDPD |
| Rh54cys | LDNKVGIQLTRIAEFTI**HQADP**AKRIHAYYITGEDPAQSDPD |
| Zn13cys | LDNKVGVQLTRIPELVL**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Rh36cys | LDNKVGIQLTRIPELVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Rh47cys | LDNKVGIQLTRIPEFVL**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Rh65cys | LDNKVGIQLTRIPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Zn71cysRT | LDNKVGLQLTRVPEFVL**QEKDP**AKQIHAYYITGEDPAQSDPD |
| ZnD3cys | LDNKVGLQLTRVPEFVL**HEKDP**AKCIHAYYITGEDPAQSDPD |
| Zn75cysRT | LDNKVGIQLTRVPEFVL**HEKDP**KKQLHAYYITGEDPAQSDPD |
| ZnA4cys | LDNKVGIQLTRVPEFVL**HEKDP**KKQLHAYYITGEDPAQSDPD |
| Cp72cys | LDNKVGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| CpF8cys | LDNKVGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| CpF9cys | LDNKVGIQLTRVPEFVI**HDKDP**AKRIHAYYITGEDPAQSDPD |
| CpC1cys | LDNKVGIQLTRVPEFVV**HEKDP**AKRIHAYYITGEDPAQSDPD |
| CpH1cys | LDNKVGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| CpD1cys | LDNQVGLQLTRVPEFVL**HEKDP**KKRIHAYYITGEDPAQFDPD |
| CpF1cys | LDNKVGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Im11cys | LDDKVGIQLTRVPEFVQ**HMSDP**AKRLHAYYITGEDPCQSDPD |
| Im42cys | LDDKAGIQLTRVPEFVQ**HESDP**AKRIHAYYITGEDPCQSDPD |
| *Treponema primitia* str. ZAS-2 fdhFcys | LSNKAGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| ZnH6cys | LSNKVGLQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |

| | |
|---|---|
| Zn9cys | LSNKAGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Zn9cysRT | LSNKAGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Zn67cysRT | LSNKAGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| ZnB9cys | LSNKAGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| *Treponema primitia* str. ZAS-1 fdhFcys | LSNKAGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Zn2cys | LSNKVGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Zn2cysRT | LSNKVGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| ZnB3cys | LSNKVGIQLTRVPEFVI**HEKDP**AKRIHAYYITGEDPAQSDPD |
| Im24cys | LSDKVGLALTRVPERVL**HEEDP**AKRIHAYYIFGEDPGQSDPD |
| Im5cys | LSDKVGLALTRVPERVL**HEEDP**AKRIHAYYIFGEDPGQSDPD |
| Cp9cys | LPEEVGLQLTRVPEKVI**HEKDP**AKRIHAYYIFGEDPAQSDPD |
| Rh93cys | LPDQPGLQLTRVPERVV**HEKDP**AKQIHAYYIFGEDPAQSDPD |
| ZnC11cys | LSPAVGLHVTRVPEFVL**DPPEE**AKRIHAYYVYGEDLAHSDPN |
| ZnH8cys | LSPTVGLHVTRVPEFVL**KEPDP**AKQIHAYYVYGEDPAHSDPN |
| CpB10sec | LSPNAGLHVTRVPEHVL**EPPSP**EKAIHGYYVYGEDPAHSDPN |
| *Clostridium bartlettii* DSM 16795 | LPSKVGLKLTEVPHAVL**E**----EHKIKAYYIFGEDPVQSDPD |
| *Clostridium difficile* 630 | LSPNNGYSLTQVPNLVL**K**----EKKLKAYYIFGEDPVQSDPD |
| *Clostridium beijerinckii* NCIMB 8052 | LSDKNGYFLTQVPELVL**K**----EDKIKAYYIFGEDPVQSDPN |
| *Clostridium carboxidivorans* P7 copy 2 | LSDKVGYHLTEVPKLVL**K**----ENKLKAYYIMGEDTVQSDPN |
| *Clostridium carboxidivorans* P7 copy 1 | LPNKVGYHLTEVPHLVL**K**----EDKIKAYYIMGEDPVQSDPD |
| *Acetonema longum* APO-1 | LPAKPGYHLTEVPHLAR-----EGKIKAYYIFGEDPVQSDPD |
| *Citrobacter koseri* ATCC BAA-895 copy 1 | LPAHTGYRISELPHRAA-----HGEVRAAYIMGEDPLQTDAE |
| *Escherichia coli* K-12 | LPAHTGYRISELPHRAA-----HGEVRAAYIMGEDPLQTDAE |
| *Buttiauxiella* SN1 | LPAHTGYRISELPHRVA-----HGEVYAAYIMGEDPLQTDAE |
| *Proteus mirabilis* HI4320 copy 1 | MPEEVGYALSEVPHNID-----HGLIKAHYVMGEDPLQTEPD |
| Cp28sec | NSREKGYPLSELPHNAI-----SGKVKAFYVMGEDPMQTEPD |
| *Yersinia frederiksenii* ATCC 33641 copy 2 | LPAHVGYSITDVPHKVA-----EGKLKAYYVFGEDPIQTEPD |
| ZnE2cys | FPEKVGLHLTEVPHAVH-----EGKLKAFYIMGEDPLQTEPD |
| *Yersinia frederiksenii* ATCC 33641 copy 1 | LSGKIGYSLTDVPHKVK-----EGKIKANYVMGEDPLQTEPD |
| *Citrobacter koseri* ATCC BAA-895 copy 2 | MDDKVGTRITEVPHLAM-----EGKIKAYYIMGEDPLQTEAD |
| *Proteus mirabilis* HI4320 copy 2 | LDPQVGYRITEVPHLAI-----EGKVKAYYIMGEDPLQTEAD |

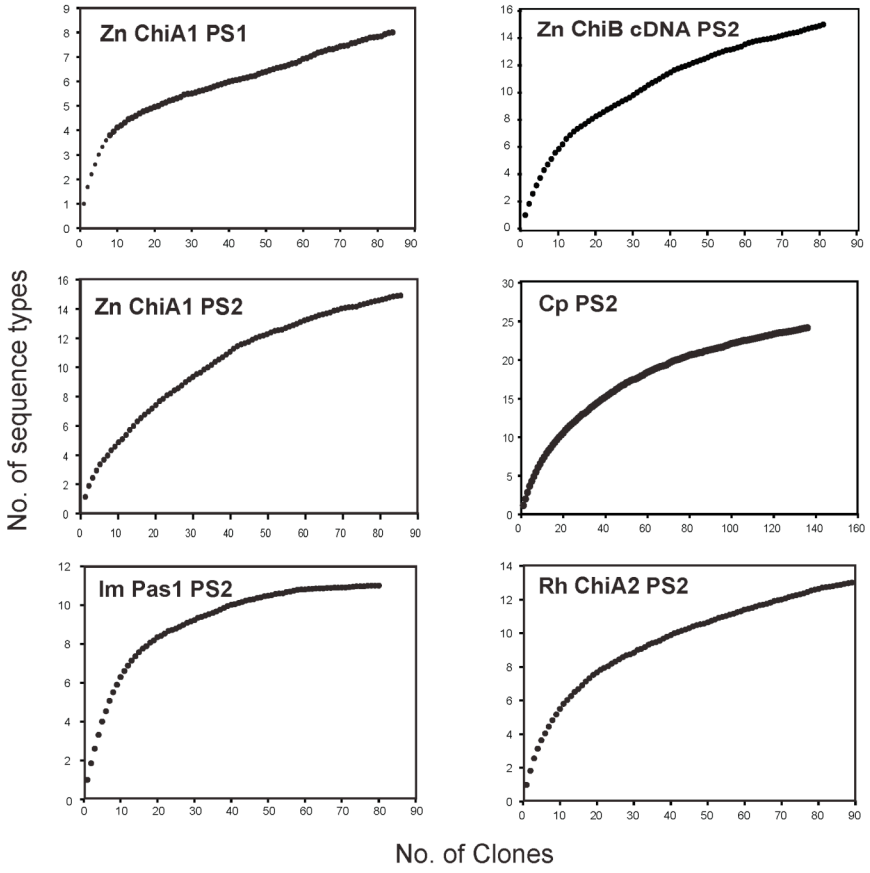
**Figure S1.** Mitochondrial cytochrome oxidase II phylogeny of insects representing major termite (*Mastotermitidae, Hodotermitidae, Termopsidae, Kalotermitidae, Rhinotermitidae, Termitidae*), wood-feeding roach (*Cryptocercidae*), and omnivorous roach (*Blattidae*) families. *Serritermitidae,* a rare group of lower termites from Brazil, is usually classified as a seventh termite family (Krishna, 1970; Grimaldi and Engel, 2005). Insects examined in this study are underlined. Families in which the wood-feeding ability has been well-established are highlighted by shaded boxes. Members of the first 5 termite families are classified as "lower" termites; those within the *Termitidae* are "higher" termites. 11 cytochrome oxidase sequences (*Amitermes dentatus* acc. no. DQ442065, *Amitermes evuncifer* DQ442066, *Cornitermes pugnax* DQ442106, *Cornitermes walkeri* AB005577, *Labiotermes labralis* DQ442149, *Microcerotermes newmani* DQ442166, *Microcerotermes parvus* DQ442167, *Nasutitermes corniger* AB037327, *Nasutitermes ephratae* AB037328, *Nasutitermes* sp. Warnecke-2007 EU236539, *Nasutitermes nigriceps* AB037329) comprise the grouped clade *Termitidae*. The tree was calculated based on 393 aligned nucleotides using the maximum likelihood algorithm AxML. Filled circles indicate nodes supported by three different tree construction methods (Fitch distance, Phylip DNA parsimony, and AxML). The scale bar represents 0.1 nucleotide changes per alignment position.

**Figure S2.** Rarefaction curves calculated using EstimateS for each insect gut *fdhF* DNA or cDNA inventory. Sequences were first binned into operational taxonomic units at a cutoff of 97% amino acid similarity (Jones-Thorton-Taylor corrected 3% amino acid difference) using DOTUR. Inventory templates (Zn, *Zootermopsis nevadensis*; Rh, *Reticulitermes hesperus*; Im, *Incistermes minor*; Cp, *Cryptocercus punctulatus*) and primer sets (PS1, primer set 1; PS2, primer set 2) are designated in the upper left corner. Primer set definitions are listed in Table S2.

**Sup. Fig. 1:**


Family Termitidae
Reticulitermes hesperus collection ChiA2 (GQ922442)
Reticulitermes hesperus (AY623447)
Reticulitermes santonensis (AF291743)
Reticulitermes speratus (AB109530)
Reticulitermes tibialis (AY168206)
Family Rhinotermitidae
Incisitermes minor collection Pas1 (GQ922441)
Incisitermes immigrans (AB109542)
Cryptotermes domesticus (AF189086)
Cryptotermes secundus (AF189093)
Kalotermes flavicollis (DQ442147)
Family Kalotermitidae
Zootermopsis nevadensis collection ChiA1 (GQ922444)
Zootermopsis nevadensis collection ChiB
Zootermopsis nevadensis (DQ493748)
Zootermopsis angusticollis (DQ442267)
Archotermopsis wroughtoni (DQ442080)
Family Termopsidae
Hodotermopsis sp. (AB018395)
Family Hodotermitidae
Mastotermes darwiniensis (AB014071)
Family Mastotermitidae
Cryptocercus clevelandi (DQ007626)
Cryptocercus punctulatus nymph (HM208251)
Cryptocercus primarius (DQ007644)
Cryptocercus relictus (AB005908)
Family Cryptocercidae
Deropeltis erythrocephala (DQ874271)
Periplaneta australasiae (DQ874310)
Periplaneta americana (HM208259 )
Family Blattidae
0.10

**Sup. Fig. 2:**


Zn ChiA1 PS1
Zn ChiB cDNA PS2
Zn ChiA1 PS2
Cp PS2
Im Pas1 PS2
Rh ChiA2 PS2
No. of sequence types
No. of Clones